

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/510,413  
Source: PCT  
Date Processed by STIC: 07-05-2005

# ***ENTERED***



PCT

## RAW SEQUENCE LISTING

DATE: 07/05/2005

PATENT APPLICATION: US/10/510,413

TIME: 11:06:25

Input Set : A:\8016-4-32448.corr-25-Nov-2003.ST25.txt

Output Set: N:\CRF4\07052005\J510413.raw

```

3 <110> APPLICANT: Novartis AG
5 <120> TITLE OF INVENTION: Compound Screening
7 <130> FILE REFERENCE: 4-32448A/NFI 8016
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/510,413
C--> 9 <141> CURRENT FILING DATE: 2004-10-06
9 <160> NUMBER OF SEQ ID NOS: 16
11 <170> SOFTWARE: PatentIn version 3.1
13 <210> SEQ ID NO: 1
14 <211> LENGTH: 326
15 <212> TYPE: PRT
16 <213> ORGANISM: human full-length sHuR
18 <220> FEATURE:
W--> 19 <221> NAME/KEY: full-length sHuR human
20 <222> LOCATION: (1)..(326)
21 <223> OTHER INFORMATION:
W--> 23 <400> 1
25 Met Ser Asn Gly Tyr Glu Asp His Met Ala Glu Asp Cys Arg Gly Asp
26 1 5 10 15
29 Ile Gly Arg Thr Asn Leu Ile Val Asn Tyr Leu Pro Gln Asn Met Thr
30 20 25 30
33 Gln Asp Glu Leu Arg Ser Leu Phe Ser Ser Ile Gly Glu Val Glu Ser
34 35 40 45
37 Ala Lys Leu Ile Arg Asp Lys Val Ala Gly His Ser Leu Gly Tyr Gly
38 50 55 60
41 Phe Val Asn Tyr Val Thr Ala Lys Asp Ala Glu Arg Ala Ile Asn Thr
42 65 70 75 80
45 Leu Asn Gly Leu Arg Leu Gln Ser Lys Thr Ile Lys Val Ser Tyr Ala
46 85 90 95
49 Arg Pro Ser Ser Glu Val Ile Lys Asp Ala Asn Leu Tyr Ile Ser Gly
50 100 105 110
53 Leu Pro Arg Thr Met Thr Gln Lys Asp Val Glu Asp Met Phe Ser Arg
54 115 120 125
57 Phe Gly Arg Ile Ile Asn Ser Arg Val Leu Val Asp Gln Thr Thr Gly
58 130 135 140
61 Leu Ser Arg Gly Val Ala Phe Ile Arg Phe Asp Lys Arg Ser Glu Ala
62 145 150 155 160
65 Glu Glu Ala Ile Thr Ser Phe Asn Gly His Lys Pro Pro Gly Ser Ser
66 165 170 175
69 Glu Pro Ile Ala Val Lys Phe Ala Ala Asn Pro Asn Gln Asn Lys Asn
70 180 185 190
73 Val Ala Leu Leu Ser Gln Leu Tyr His Ser Pro Ala Arg Arg Phe Gly
74 195 200 205
77 Gly Pro Val His His Gln Ala Gln Arg Phe Arg Phe Ser Pro Met Gly

```

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```

78      210      215      220
81 Val Asp His Met Ser Gly Leu Ser Gly Val Asn Val Pro Gly Asn Ala
82 225      230      235      240
85 Ser Ser Gly Trp Cys Ile Phe Ile Tyr Asn Leu Gly Gln Asp Ala Asp
86      245      250      255
89 Glu Gly Ile Leu Trp Gln Met Phe Gly Pro Phe Gly Ala Val Thr Asn
90      260      265      270
93 Val Lys Val Ile Arg Asp Phe Asn Thr Asn Lys Cys Lys Gly Phe Gly
94      275      280      285
97 Phe Val Thr Met Thr Asn Tyr Glu Glu Ala Ala Met Ala Ile Ala Ser
98      290      295      300
101 Leu Asn Gly Tyr Arg Leu Gly Asp Lys Ile Leu Gln Val Ser Phe Lys
102 305      310      315      320
105 Thr Asn Lys Ser His Glu
106      325

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109 &lt;210&gt; SEQ ID NO: 2

110 &lt;211&gt; LENGTH: 325

111 &lt;212&gt; TYPE: PRT

112 &lt;213&gt; ORGANISM: Homo sapiens

114 &lt;220&gt; FEATURE:

W--&gt; 115 &lt;221&gt; NAME/KEY: sHuR

116 &lt;222&gt; LOCATION: (2)..(325)

117 &lt;223&gt; OTHER INFORMATION:

W--&gt; 119 &lt;400&gt; 2

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121 Ser Asn Gly Tyr Glu Asp His Met Ala Glu Asp Cys Arg Gly Asp Ile
122 1      5      10      15
125 Gly Arg Thr Asn Leu Ile Val Asn Tyr Leu Pro Gln Asn Met Thr Gln
126      20      25      30
129 Asp Glu Leu Arg Ser Leu Phe Ser Ser Ile Gly Glu Val Glu Ser Ala
130      35      40      45
133 Lys Leu Ile Arg Asp Lys Val Ala Gly His Ser Leu Gly Tyr Gly Phe
134      50      55      60
137 Val Asn Tyr Val Thr Ala Lys Asp Ala Glu Arg Ala Ile Asn Thr Leu
138 65      70      75      80
141 Asn Gly Leu Arg Leu Gln Ser Lys Thr Ile Lys Val Ser Tyr Ala Arg
142      85      90      95
145 Pro Ser Ser Glu Val Ile Lys Asp Ala Asn Leu Tyr Ile Ser Gly Leu
146      100      105      110
149 Pro Arg Thr Met Thr Gln Lys Asp Val Glu Asp Met Phe Ser Arg Phe
150      115      120      125
153 Gly Arg Ile Ile Asn Ser Arg Val Leu Val Asp Gln Thr Thr Gly Leu
154      130      135      140
157 Ser Arg Gly Val Ala Phe Ile Arg Phe Asp Lys Arg Ser Glu Ala Glu
158 145      150      155      160
161 Glu Ala Ile Thr Ser Phe Asn Gly His Lys Pro Pro Gly Ser Ser Glu
162      165      170      175
165 Pro Ile Ala Val Lys Phe Ala Ala Asn Pro Asn Gln Asn Lys Asn Val
166      180      185      190
169 Ala Leu Leu Ser Gln Leu Tyr His Ser Pro Ala Arg Arg Phe Gly Gly

```

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```

170          195          200          205
173 Pro Val His His Gln Ala Gln Arg Phe Arg Phe Ser Pro Met Gly Val
174          210          215          220
177 Asp His Met Ser Gly Leu Ser Gly Val Asn Val Pro Gly Asn Ala Ser
178 225          230          235          240
181 Ser Gly Trp Cys Ile Phe Ile Tyr Asn Leu Gly Gln Asp Ala Asp Glu
182          245          250          255
185 Gly Ile Leu Trp Gln Met Phe Gly Pro Phe Gly Ala Val Thr Asn Val
186          260          265          270
189 Lys Val Ile Arg Asp Phe Asn Thr Asn Lys Cys Lys Gly Phe Gly Phe
190          275          280          285
193 Val Thr Met Thr Asn Tyr Glu Glu Ala Ala Met Ala Ile Ala Ser Leu
194          290          295          300
197 Asn Gly Tyr Arg Leu Gly Asp Lys Ile Leu Gln Val Ser Phe Lys Thr
198 305          310          315          320

```

201 Asn Lys Ser His Glu

202 325

205 &lt;210&gt; SEQ ID NO: 3

206 &lt;211&gt; LENGTH: 189

207 &lt;212&gt; TYPE: PRT

208 &lt;213&gt; ORGANISM: Homo sapiens

210 &lt;220&gt; FEATURE:

W--&gt; 211 &lt;221&gt; NAME/KEY: HuR12

212 &lt;222&gt; LOCATION: (1)..(189)

213 &lt;223&gt; OTHER INFORMATION:

W--&gt; 215 &lt;400&gt; 3

```

217 Met Ser Asn Gly Tyr Glu Asp His Met Ala Glu Asp Cys Arg Gly Asp
218 1          5          10          15
221 Ile Gly Arg Thr Asn Leu Ile Val Asn Tyr Leu Pro Gln Asn Met Thr
222          20          25          30
225 Gln Asp Glu Leu Arg Ser Leu Phe Ser Ser Ile Gly Glu Val Glu Ser
226          35          40          45
229 Ala Lys Leu Ile Arg Asp Lys Val Ala Gly His Ser Leu Gly Tyr Gly
230          50          55          60
233 Phe Val Asn Tyr Val Thr Ala Lys Asp Ala Glu Arg Ala Ile Asn Thr
234 65          70          75          80
237 Leu Asn Gly Leu Arg Leu Gln Ser Lys Thr Ile Lys Val Ser Tyr Ala
238          85          90          95
241 Arg Pro Ser Ser Glu Val Ile Lys Asp Ala Asn Leu Tyr Ile Ser Gly
242          100          105          110
245 Leu Pro Arg Thr Met Thr Gln Lys Asp Val Glu Asp Met Phe Ser Arg
246          115          120          125
249 Phe Gly Arg Ile Ile Asn Ser Arg Val Leu Val Asp Gln Thr Thr Gly
250          130          135          140
253 Leu Ser Arg Gly Val Ala Phe Ile Arg Phe Asp Lys Arg Ser Glu Ala
254 145          150          155          160
257 Glu Glu Ala Ile Thr Ser Phe Asn Gly His Lys Pro Pro Gly Ser Ser
258          165          170          175
261 Glu Pro Ile Ala Val Lys Phe Ala Ala Asn Pro Asn Gln

```



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7/5/05

RAW SEQUENCE LISTING ERROR SUMMARY      DATE: 07/05/2005  
PATENT APPLICATION:    US/10/510,413      TIME: 11:06:26

Input Set : A:\8016-4-32448.corr-25-Nov-2003.ST25.txt  
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,  
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:11,12,13,14,15,16

## VERIFICATION SUMMARY

DATE: 07/05/2005

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TIME: 11:06:26

Input Set : A:\8016-4-32448.corr-25-Nov-2003.ST25.txt

Output Set: N:\CRF4\07052005\J510413.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No  
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:19 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1  
L:23 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:21  
L:115 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2  
L:119 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:117  
L:211 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3  
L:215 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:213  
L:271 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4  
L:275 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:273  
L:331 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5  
L:335 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:333  
L:345 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6  
L:349 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:347  
L:359 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7  
L:363 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:361  
L:373 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8  
L:377 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:375  
L:387 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9  
L:391 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:389  
L:401 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10  
L:405 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:10,Line#:403